

Development of novel SNP assays for genetic analysis of rare minnow (*Gobiocypris rarus*) in a successive generation closed colony

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Supplemental material

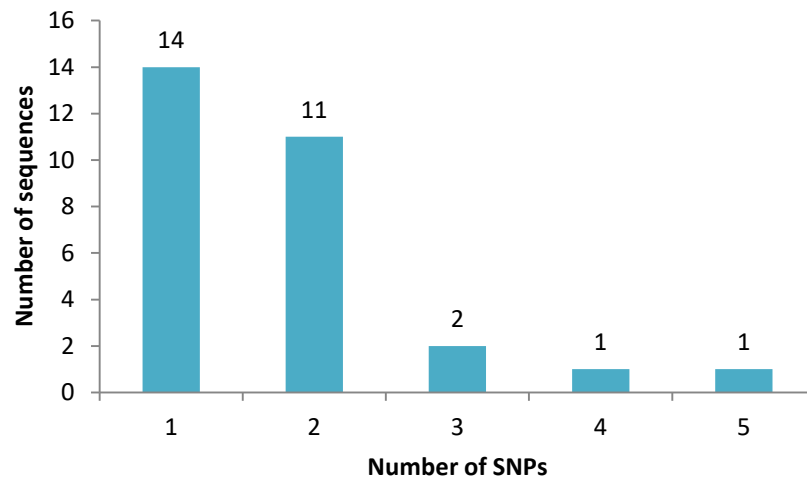


Figure S1. Frequency distribution of 51 SNPs in 29 sequences

Table S1. Characterization of 51 SNP markers in the rare minnow

Loci	Type	Primer sequence (5'-3')	Extension primer	Extension product	Tm/ °C	Extension length	Position	Annotation
Seq2	A/G	AGCTGCTAGTGAGGTAAACAC	TGGAGAAATGTTAACATTCT	24RCT	51	87bp	Seq2 +789	Rhinoceros 28S ribosomal protein
		ACCTTTCCACAGTCTGATTGG	ATT					

Seq3	C/G	CGCTTGGATTTCGCATTCTC TCAGTATTGCCGACACTGTATT	ctgactgactgactgactgactgCTCTCT TCAACGCTCTTTGTGTTCT	47FCG	55	91bp	Seq3 +1001	Vascular endothelial growth factor A-A-like
Seq4	C/G	TGGATCTCACGCGCTCTC ACACGGGGTCCGACCTATA	ctgactgactgactgactgactgactgCT CTCAGGTGTCTGCATGCGTGT T	54FCG	57	88bp	Seq4 +1001	Vascular endothelial growth factor A-A-like
Seq5	A/C	ATGTGTGTTGATTGCTGATTGAT GCCACAGCTCAAAGTCTACA	AAAGTCTAAAGGAAACCGTC AAAA	24RGT	53	105bp	Seq5 +1001	/
Seq7	A/G	TTAAAGGTGGTGCGACTTG AGTTCCTGTATTCTGCTTGTATT	ctgactgactgaCTATTGTTCATC TTTGTAAACA	36RCT	53	116bp	Seq7 +824	Non-muscle caldesmon-like
Seq9	G/T	CAAATAAGACCTCCGTGGCTTT AACAGGTGGAAGAGGAGGAG	ctgactgactgaCACACCACCTCC TCCCTACGGAT	36FGT	55	80bp	Seq9 +954	Non-muscle caldesmon-like
Seq10-1	A/G	CCGCTACATACATCCCTTCCA TGATTGATAACCTTTCTGCTGCG	ctgactCCGCACCGCCTTCACCC ACGGTGCG	30FAG	60	176bp	Seq10 +1001	Vascular endothelial growth factor Ab (vegfab)
Seq10-2	C/T	Same as Seq10-1	ctgactgactgactgactCACATCTCA AGGATCTGCTGCAGA	42FCT	60	176bp	Seq10 +1086	Transmembrane protein 168-A
Seq11-1	C/G	GAGTCCTCCAGGAATGATGA ATGAATACAACACATAATTGACCC C	ctgactgactgactgactgactgaTCGTG CGTGGTGCCCTGTAATAGG	48RCG	54	371bp	Seq11 +1001	Forkhead box P2
Seq11-2	A/T	Same as Seq11-1	ctgactgactgactgaCGTTAGTGTC CAGGTGATCTAGTG	40RAT	54	371bp	Seq11 +1039	Forkhead box P2
Seq11-3	A/T	Same as Seq11-1	ctgactgactgactgactgaAAAAAAG GCCATTTGAAAAAGTAT	44FAT	54	371bp	Seq11 +1310	/
Seq12	A/G	AACAAAAGGACAAGACTTCATTC G CTCGCTCCCGTTTCACTTC	ATCAGCTTGGCCACCTCACAC CAAC	24FAG	58	99bp	Seq12 +1001	Forkhead box protein P2-like
Seq13-1	G/C	GAGGCTTAGGCGAGTCAAT CTCATTTGTCAGCACTTACTTCT	ctgactgactgactgactgactgactgA ATATTGGCCTTTTGCATGCTT GG	54FCG	54	250bp	Seq13 +866	MyoD family inhibitor domain-containing protein-like
Seq13-2	A/T	Same as Seq13-1	ctgactgactgactgactgactgTCC GATACCAGGAGATCACACTT C	51FAT	54	250bp	Seq13 1001	MyoD family inhibitor domain-containing protein-like
Seq13-3	A/C	Same as Seq13-1	ctgactgaGCAGGGTCACATGAT CGGGGAGAA	32FAC	54	250bp	Seq13 +1031	MyoD family inhibitor domain-containing protein-like
Seq15-1	A/C	CCTCCAAAGCCCGTCTCC CGAAGTGAAGAAAACCTCAGC	ctgactgactgactgactgactgactgTC CAATCAAAGTCGAGAAGCAG	54FAC	56	172bp	Seq15 +1001	ETS

			CG						domain-containing
									protein Elk-3-like
									protein
Seq15-2	G/C	Same as Seq15-1	ctgactgactgactGTCGTTCCCCTT GCTTCCTCACCA	38FGC	56	172bp	Seq15 +1089	ELK3, ETS transcription factor	
Seq18-1	A/G	ACAGCCGTTTGTTATTTTGACA GCAATTCAGTGTGTGTGATCC	ctgactgactgactAATTCTTATAAA ACTACAACTATG	38FAG	55	104bp	Seq18 +897	Phytanoyl-CoA 2-hydroxylase	
Seq18-2	A/G	Same as Seq18-1	CATGATTTACTCGCTACAGTG CCA	25RCT	55	104bp	Seq18 +911	Phytanoyl-CoA 2-hydroxylase	
Seq26-1	C/T	GCAACTGTTAATTTCTAATTACCC TTACCTATTGGTCATTTGGAACC	ctgactgactATGCCACCCTTTAA AAAAAGAACA	34FCT	59	488bp	Seq26 +1001	La-related protein 4-like	
Seq26-2	A/C/T	Same as Seq26-1	ctgactgactgactgactgactTCGC ACAGAAATAGTCACAGAAAT	50FACT	59	488bp	Seq26 +1392	La-related protein 4-like	
Seq27	A/T	GCCTGGGGACAGTCTCCT TCTCCAGCAGCAGGATTCAAG	ctgactgactgaCCTCTGAGGCTGG GCTTGCGGG	34FAT	56	77bp	Seq27 +1001	La-related protein 4-like	
								Limb development	
Seq28	C/T	ACCAAATAACCAAATGTACTGTT CCTCTAGGCATAGCAGATTCA	GGTGTGTGTGCTGATGGTCTG TTT	24FCT	53	102bp	Seq28 +1001	membrane protein 1 like	
Seq29	C/T	CAGTTGGGCACATTTGGC CTATGATCTGGTCCCCTCTGA	ctgactgactgaTAGTCTCTGGTCA CAAACCACCTT	36FCT	56	87bp	Seq29 +1001	Idella activin receptor type IB	
Seq30	C/T	GTCCCTGCCACCAGAGAA GCTGGCACTGCACAAATGA	ctgactgactgactgactaTCCCTGCC TAATGTCTTCAGCGCC	44FCT	55	97bp	Seq30 +1001	E3 ubiquitin-protein ligase HUWE1-like	
Seq31-1	C/T	CGTCCAAATGTGCAGGTCT GGGGTCCAGTCCAAAATACTC	ctgactgactgactgactgactgaTTT GGTTTCTCAGGTGTACAACA	52FCT	56	272bp	Seq31 +819	/	
Seq31-2	C/T	Same as Seq31-1	ctgactgactgactgactgactGTACAA CAYGAGACCAAATTTTAA	46FCT	56	272bp	Seq31 +835	/	
Seq31-3	A/G	Same as Seq31-1	TTTTAAYCATCGAATGAATTG CC	23FAG	56	272bp	Seq31 +852	Transient receptor potential cation	

									channel subfamily A member 1-like
									Transient receptor potential cation channel subfamily A member 1-like
Seq31-4	C/T	Same as Seq31-1	ctgactgactgactgaTTAGAGTAGA TTAAACTTTGAAAT	40RAG	56	272bp	Seq31 +855		Serine
Seq31-5	A/G	Same as Seq31-1	ctgactgactgactgactgactgaTCATA GTATTGGGGCATTAGGACC	48FAG	56	272bp	Seq31 +1001		palmitoyltransferase
									2-like
Seq36-1	C/T	AAGGTGTGCTGGGGTCTT CCACTTTTCCTGTTTCTGTTCCTC	ctgactgaAGGAATGCTCTCCAT ATGCTGCTC	32RAG	54	81bp	Seq36 +36		/
Seq36-2	A/C	TTATTATTGTGCAGTCAACCA ATCGGATAATGGATAACTTCG	TCACCTGACAAATCAGATCC TGAA	24FAC	54	102bp	Seq36 +1001		HHIP-like protein 1
		TTGTAATGAGGCTCCAAATTGA							/
Seq37	C/G	TGGAAAGGAATATGATCAGACTA T	ctgactCTGTAAATACACATTG ACAGTAT	30FCG	54	97bp	Seq37 +733		Histone-lysine
Seq38-1	G/T	CGCAAACCTGGAAGAAGAAGAC TTAAGAACAGGGGATTGGAGTC	AGACGAGAATGTTCAAGGAGG AGAT	24FGT	56	101bp	Seq38 +1001		N-methyltransferase
									setd3
									Histone-lysine
Seq38-2	A/G	Same as Seq38-1	ctgactgactgactgactgactGGCAGG CAGCGTCGGGCTTGATTT	46RCT	56	101bp	Seq38 +1011		N-methyltransferase
									setd3
Seq39-1	C/G	CAATAAACCTGTGCTGAAACT ACCAGAAGTAAGTACTCCAGAA A	ctgactgactgactgactgactgactCT CTTGATGAACGTCCAGCCCC A	54FCG	52	144bp	Seq39 +1001		Solute carrier family 22 member 15-like
Seq39-2	C/T	Same as Seq39-1	ctgactgactgaGCGAATCTTAGAG CCACAGGTGAA	36FCT	52	144bp	Seq39 +1032		/
		ATGGAAGGCGCCAATATATGAT							/
Seq42-1	G/T	T ACCTCTGGAACGCATGAATA	ctgactgactgactgaCAAGAATATG CCTGGGCCATATTT	40RAC	55	161bp	Seq42 +648		
Seq42-2	G/T	Same as Seq42-1	ctgactTATAAAGTAGGTAAATC TAAATCA	30RAC	55	161bp	Seq42 +682		/
		TTTACTCTCTCCTTAGGTGTCTT							Kinesin-like protein
Seq43	A/C	AGAACAGACAAATCATGTTGAA AG	ctgactgactgaAAAGACATACAC AGAAGTTAAAA	36RGT	56	75bp	Seq43 +1001		KIF11
Seq46-1	A/T	ATGCTAGAGTGTGAATTGTGG TCTATGACATCATTTTCAGTTGT	ctgactgactgactgactgaATACATTT CGAACACAATTTTTTT	44FAT	51	107bp	Seq46 +689		/
Seq46-2	A/T	Same as Seq46-1	ctgactgactgactgactgactgTGTG	51RAT	51	107bp	Seq46 +693		/

			CCTCCTTTCATAAAAAAATT						
Seq49	A/G	TCATAACCAATCTGTCATTCTTGT TTAGTTTGGGACTCAACTCTGAT	ctgactgactgactgactgactgactgT ACTAAACTGAATTTAGCTTAT T	54FAG	55	90bp	Seq49 +1212	/	
Seq50-1	A/T	GCTTCTTAATCTGCTGCAAATAGT TGATTACTTGCATAAGGCAACCT T	ctgactgactgactgactgactCATA AAATAACATATTTATCATTAA	50FAT	57	479bp	Seq50 +694	/	
Seq50-2	A/G	Same as Seq50-1	ctgactGTATCACTATCCTTATG CGGTGCC	30FAG	57	479bp	Seq50 +1001	/	
Seq51-1	A/G	GCGGAGTAAATAAGTGAATGA TT AATTATCCACAATGAGCATGTCG	GTATGTAAACAGCTAAAATT TATG	24RCT	57	385bp	Seq51 +846	/	
Seq51-2	A/G	Same as Seq51-1	CCACTGGTTGTCATGGAGAG CTCG	24FAG	57	385bp	Seq51 +1001		Neurexin-3a
Seq51-3	A/G	Same as Seq51-1	ctgactgactgactgaCTTGATTACAT TGGGCCCGTTGCC	40FAG	57	385bp	Seq51 +1037		Neurexin-3a
Seq51-4	G/C	Same as Seq51-1	ctgactgagactgagactgactCTATATT CCATTCCAAATCTCTCA	46FGC	57	385bp	Seq51 +1139	/	
Seq53-1	A/G	ATGGCAAAGTCATGTCAGATGTA G GTCTGGAGGAGCAGGCAG	ctgactgactgactgactgactTTGA TGAAGAAACACGGCCGTATC	50FAG	55	210bp	Seq53 +882	/	
Seq53-2	C/T	Same as Seq53-1	ctgactgactgactgactgactgactC CGATCTGTGCGTGGTGAACG CGA	54FCT	55	210bp	Seq53 +1001		Protein phosphatase 1 regulatory subunit 37-like